

## BLAST Basic Local Alignment Search Tool

Job Title: Nucleotide sequence (238 letters)

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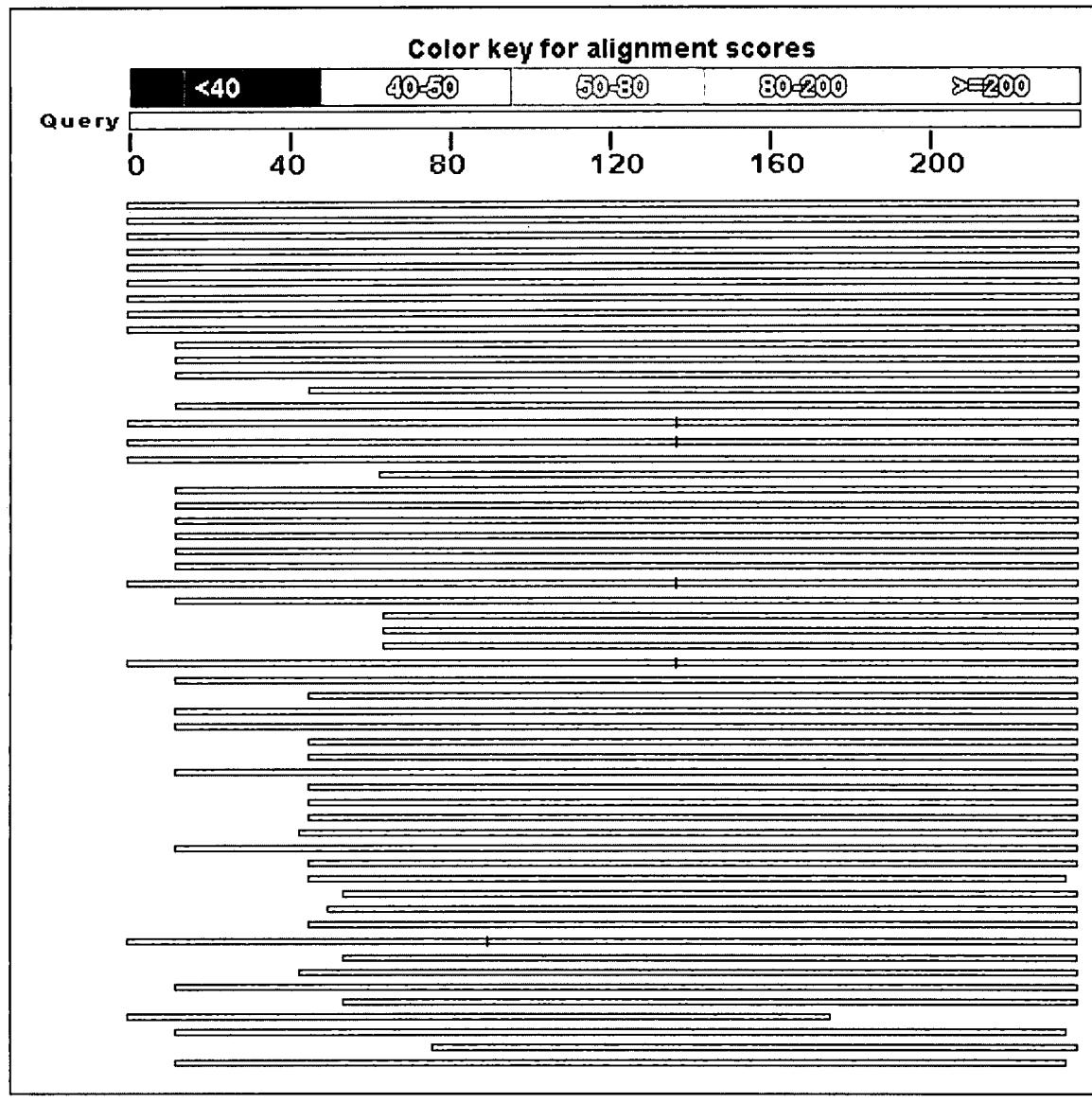
BLASTN 2.2.16 (Mar-25-2007)

RID: 7ZDFWYZJ014 Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
5,413,143 sequences; 20,916,285,690 total letters

Query= Length=238

*bases 756 - 793 of SEQ ID NO:2 (3' UTR of HCV1a)*

## Distribution of 105 Blast Hits on the Query Sequence



## Distance tree of results NEW

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Struct

## Sequences producing significant alignments:

(Click headers to sort columns)

AF271632.1	Hepatitis C virus polyprotein gene, complete cds	318	318	100%	5e- 84	90%
AF009072.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #74	316	316	100%	2e- 83	90%
AF177040.1	Synthetic construct clone pH77(p7)-J6S hepatitis C virus, complete genome	300	300	100%	2e- 78	90%
AF177039.1	Synthetic construct clone pH77-J6S hepatitis C virus, complete genome	300	300	100%	2e- 78	90%
AF177038.1	Synthetic construct clone pH77(p7)CV-J6S hepatitis C virus, complete genome	300	300	100%	2e- 78	90%
AF177037.1	Synthetic construct clone pH77CV-J6S hepatitis C virus, complete genome	300	300	100%	2e- 78	90%
AF011753.1	Hepatitis C virus strain H77 pH21 polyprotein gene, complete cds	300	300	100%	2e- 78	90%
AF011752.1	Hepatitis C virus strain H77 pCV-H11 polyprotein gene, complete cds	300	300	100%	2e- 78	90%
AF011751.1	Hepatitis C virus strain H77 pCV-H77C polyprotein gene, complete cds	300	300	100%	2e- 78	90%
AY045702.1	Hepatitis C virus isolate HCR6, complete genome	296	296	94%	2e- 77	90%
AF139594.2	Hepatitis C virus strain HCV-N, complete genome	294	294	94%	8e- 77	90%
AB119282.1	Hepatitis C virus gene for Fusion protein, Feo, complete cds	289	289	94%	4e- 75	90%
D84265.2	Hepatitis C virus (isolate VN004) genomic RNA, complete genome	272	272	81%	4e- 70	92%
AB049089.1	Hepatitis C virus gene for polyprotein, complete cds, isolate: HCVT109	272	272	94%	4e- 70	88%
AF387806.1	Synthetic construct HCV type 1a polyprotein mRNA, complete cds	270	426	100%	1e- 69	91%
AF009606.1	Hepatitis C virus polyprotein gene, complete cds	270	426	100%	1e- 69	91% <b>G</b>
AF009070.1	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #8	270	270	100%	1e- 69	88%
AF333324.1	Hepatitis C virus type 1b polyprotein mRNA, complete cds	267	267	73%	2e- 68	94%
AF356827.1	Hepatitis C virus isolate HCV-S1, complete genome	263	263	94%	2e- 67	87%
AB049090.1	Hepatitis C virus gene for polyprotein, complete cds, isolate: HCVT140	261	261	94%	8e- 67	88%
D85021.1	Hepatitis C virus genomic RNA for 3'UTR	261	261	94%	8e- 67	87%
AF387808.1	Synthetic construct HCV type 1a/1b chimera mutant polyprotein mRNA, complete cds	259	259	94%	3e- 66	88%
AF387807.1	Synthetic construct HCV type 1a/1b	259	259	94%	3e-	88%

	chimera polyprotein mRNA, complete cds				66
<b>AF387805.1</b>	Synthetic construct HCV type 1a/1b chimera polyprotein mRNA, complete cds	259	259	94%	3e- 88% 66
<b>S82227.1</b>	Hepatitis C virus NS5B (NS5B) gene, partial cds	259	415	100%	3e- 90% 66
<b>D63922.1</b>	Hepatitis C virus genomic RNA, 3' UTR	259	259	94%	3e- 87% 66
<b>AF054249.1</b>	Hepatitis C virus HC-J4, pCV-J4L4S, complete genome	259	259	73%	3e- 93% 66
<b>AF054248.1</b>	Hepatitis C virus HC-J4, pCV-J4L2S, complete genome	259	259	73%	3e- 93% 66
<b>AF054247.1</b>	Hepatitis C virus HC-J4, pCV-J4L6S, complete genome	259	259	73%	3e- 93% 66
<b>AF009071.1</b>	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #10	259	415	100%	3e- 90% 66
<b>AB049088.1</b>	Hepatitis C virus genomic RNA, complete genome, isolate: HCVT094	257	257	94%	1e- 87% 65
<b>D84263.2</b>	Hepatitis C virus (isolate VN235) genomic RNA, complete genome	255	255	81%	4e- 90% 65
<b>D67094.1</b>	Hepatitis C virus genomic RNA, 3' terminus partial sequence, clone: #12	255	255	94%	4e- 87% 65
<b>AF176573.1</b>	Hepatitis C virus polyprotein precursor, gene, complete cds	254	254	94%	1e- 87% 64
<b>AB049101.1</b>	Hepatitis C virus gene for polyprotein, complete cds, isolate: HCVT221	254	254	81%	1e- 90% 64
<b>AF009076.1</b>	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #27	254	254	81%	1e- 90% 64
<b>D85020.1</b>	Hepatitis C virus genomic RNA for 3'UTR	254	254	94%	1e- 87% 64
<b>AB049095.1</b>	Hepatitis C virus gene for polyprotein, complete cds, isolate: HCVT169	252	252	81%	5e- 90% 64
<b>AB049091.1</b>	Hepatitis C virus gene for polyprotein, complete cds, isolate: HCVT142	250	250	81%	2e- 90% 63
<b>AB047645.1</b>	Hepatitis C virus gene for polyprotein, complete cds, clone: JCH-6	250	250	81%	2e- 89% 63
<b>D85025.1</b>	Hepatitis C virus genomic RNA for 3'UTR	248	248	81%	6e- 90% 63
<b>D85022.1</b>	Hepatitis C virus genomic RNA for 3'UTR	246	246	94%	2e- 86% 62
<b>AF169003.1</b>	Hepatitis C virus isolate G2aK1 polyprotein gene, complete cds	243	243	81%	3e- 89% 61
<b>AF009075.1</b>	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #16	243	243	79%	3e- 89% 61
<b>D85024.1</b>	Hepatitis C virus genomic RNA for 3'UTR	243	243	77%	3e- 90% 61
<b>D67092.1</b>	Hepatitis C virus genomic RNA, 3' terminus partial sequence, clone: #6	243	243	78%	3e- 90% 61
<b>AF177036.1</b>	Hepatitis C virus clone pJ6CF, complete genome	241	241	81%	1e- 89% 60
<b>AF009069.1</b>	Hepatitis C virus genomic RNA, 3' nontranslated region, partial	241	340	100%	1e- 94% 60

sequence. clone #1.2

<b>AB191333.1</b>	Hepatitis C virus genomic RNA, complete genome, strain:0	239	239	77%	4e- 60	90%
<b>D84264.2</b>	Hepatitis C virus (isolate VN405) genomic RNA, complete genome	239	239	81%	4e- 60	89%
<b>AJ278830.1</b>	Hepatitis C virus genomic RNA for polyprotein gene	239	239	94%	4e- 60	86%
<b>AB080299.1</b>	Hepatitis C virus genomic RNA, complete genome, isolate:MLE	239	239	77%	4e- 60	90%
<b>AF009073.1</b>	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #5	239	239	73%	4e- 60	91%
<b>DQ071885.1</b>	Hepatitis C virus polyprotein mRNA, complete cds	237	237	93%	1e- 59	86%
<b>AY460204.1</b>	Hepatitis C virus from Shanghai, complete genome	237	237	68%	1e- 59	93%
<b>AJ238799.1</b>	Hepatitis C virus type 1b complete genome, isolate Con1	237	237	93%	1e- 59	86%
<b>AJ242651.1</b>	Hepatitis C virus replicon I377/NS2- 3'UTR	237	237	93%	1e- 59	86%
<b>AJ242654.1</b>	Hepatitis C virus replicon I389/NS3- 3'UTR	237	237	93%	1e- 59	86%
<b>AJ242653.1</b>	Hepatitis C virus replicon I389/NS2- 3'UTR	237	237	93%	1e- 59	86%
<b>AJ242652.1</b>	Hepatitis C virus replicon I377/NS3- 3'UTR	237	237	93%	1e- 59	86%
<b>AF009074.1</b>	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #19	237	237	73%	1e- 59	91%
<b>D85023.1</b>	Hepatitis C virus genomic RNA for 3'UTR	237	237	73%	1e- 59	91%
<b>D85018.1</b>	Hepatitis C virus genomic RNA for 3'UTR	235	235	73%	5e- 59	91%
<b>D67091.1</b>	Hepatitis C virus genomic RNA, 3'terminus partial sequence, clone: 1090CONS	235	235	69%	5e- 59	92%
<b>D84262.2</b>	Hepatitis C virus (isolate Th580) genomic RNA, complete genome	231	231	81%	6e- 58	88%
<b>AB047644.1</b>	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-5	230	230	81%	2e- 57	88%
<b>D85019.1</b>	Hepatitis C virus genomic RNA for 3'UTR	230	230	73%	2e- 57	91%
<b>D85016.1</b>	Hepatitis C virus genomic RNA for 3'UTR	230	230	73%	2e- 57	91%
<b>AF169005.1</b>	Hepatitis C virus isolate NDM59 polyprotein gene, complete cds	228	228	81%	8e- 57	88%
<b>D85017.1</b>	Hepatitis C virus genomic RNA for 3'UTR	228	228	72%	8e- 57	91%
<b>AF169002.1</b>	Hepatitis C virus isolate NDM228 polyprotein gene, complete cds	226	226	78%	3e- 56	89%
<b>D85026.1</b>	Hepatitis C virus genomic RNA for 3'UTR	226	226	81%	3e- 56	88%
<b>D67096.1</b>	Hepatitis C virus genomic RNA, 3'terminus partial sequence, clone: 72CONS	226	226	80%	3e- 56	88%
<b>AB237837.1</b>	Hepatitis C virus full-length replicon pFGR-JFH1 RNA, complete sequence	224	224	81%	1e- 55	87%

<b>AB047639.1</b>	Hepatitis C virus (isolate JFH-1) genomic RNA, complete genome	224	224	81%	1e- 55	87%
<b>AB114136.1</b>	Hepatitis C virus replicon pSGR-JFH1 gene for neomycin resistance gene product, hepatitis C virus nonstructural protein, complete cds	224	224	81%	1e- 55	87%
<b>D67095.1</b>	Hepatitis C virus genomic RNA, 3'terminus sequence	219	219	72%	5e- 54	89%
<b>AB030907.1</b>	Hepatitis C virus (isolate JPUT971017) genomic RNA, complete genome	217	217	73%	2e- 53	89%
<b>AY746460.1</b>	Hepatitis C virus genotype 2a polyprotein gene, complete cds	215	215	81%	6e- 53	87%
<b>AF169004.1</b>	Hepatitis C virus isolate G2aK3 polyprotein gene, complete cds	215	215	73%	6e- 53	89%
<b>AB047640.1</b>	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-1	215	215	81%	6e- 53	87%
<b>AB047642.1</b>	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-3	206	206	82%	4e- 50	85%
<b>AB047641.1</b>	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-2	206	206	71%	4e- 50	88%
<b>D67093.1</b>	Hepatitis C virus genomic RNA, 3'terminus partial sequence, clone: #9	202	202	63%	5e- 49	92%
<b>AF009077.1</b>	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #23	198	198	62%	7e- 48	91%
<b>AB047643.1</b>	Hepatitis C virus gene for polyprotein, complete cds, clone:JCH-4	193	193	65%	3e- 46	88%
<b>AB001040.1</b>	Hepatitis C virus (subtype:1b) genomic RNA for polyprotein and 3'UTR, partial cds	193	193	51%	3e- 46	95%
<b>AB016785.1</b>	Hepatitis C virus genomic RNA, complete sequence	191	191	48%	1e- 45	96%
<b>D89815.1</b>	Hepatitis C virus genomic RNA, complete sequence	189	189	58%	4e- 45	91%
<b>D85516.1</b>	Hepatitis C virus genomic RNA, complete cds	187	187	51%	1e- 44	94%
<b>AJ132997.1</b>	Hepatitis C virus, complete genome, isolate HCV-AD78P1	183	183	52%	2e- 43	92%
<b>DQ321850.1</b>	Hepatitis C virus isolate plasma X clone 20 X-tail 3' UTR	176	176	41%	3e- 41	98%
<b>DQ321849.1</b>	Hepatitis C virus isolate plasma X clone 19 X-tail 3' UTR	176	176	41%	3e- 41	98%
<b>DQ321848.1</b>	Hepatitis C virus isolate plasma X clone 18 X-tail 3' UTR	176	176	41%	3e- 41	98%
<b>DQ321847.1</b>	Hepatitis C virus isolate plasma X clone 17 X-tail 3' UTR	176	176	41%	3e- 41	98%
<b>DQ321846.1</b>	Hepatitis C virus isolate plasma X clone 16 X-tail 3' UTR	176	176	41%	3e- 41	98%
<b>DQ321845.1</b>	Hepatitis C virus isolate plasma X clone 15 X-tail 3' UTR	176	176	41%	3e- 41	98%
<b>DQ321844.1</b>	Hepatitis C virus isolate plasma X clone 14 X-tail 3' UTR	176	176	41%	3e- 41	98%
<b>DQ321843.1</b>	Hepatitis C virus isolate plasma X clone 13 X-tail 3' UTR	176	176	41%	3e- 41	98%
<b>DQ321842.1</b>	Hepatitis C virus isolate plasma X clone 12 X-tail 3' UTR	176	176	41%	3e- 41	98%

## Alignments

>gb|AF271632.1|AF271632 Hepatitis C virus polyprotein gene, complete cds  
Length=9618

Score = 318 bits (172), Expect = 5e-84  
Identities = 223/246 (90%), Gaps = 10/246 (4%)  
Strand=Plus/Plus

Query 116 c-ttttctttttt--cttctttAATGGTGGCTCCATCTAGCCCTAGTCACGGCTAG  
Sbjct 9495 .T.....T.T.....CC...-.-.....

Query 233 TCATGT 238  
Sbjct 9613 ..... 9618

>gb|AF009072.1|AF009072 Hepatitis C virus genomic RNA, 3' nontranslated r  
sequence. clone #74  
Length=321

Score = 316 bits (171), Expect = 2e-83  
Identities = 222/244 (90%), Gaps = 13/244 (5%)  
Strand=Plus/Plus

Query 120 t-c--tcttt--tttcttcttAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCT 1  
Sbjct 198 .C.TT.....CC..C..... 2

Query 175 GTGAAAGGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTCTGCAGATC 2  
Sbjct 258 .....G.....T..... 3

Query 235 ATGT 238  
Sbjct 318 .... 321

>gb|AF177040.1| Synthetic construct clone pH77(p7)-J6S hepatitis C virus, genome  
Length=9611

Score = 300 bits (162), Expect = 2e-78  
Identities = 215/238 (90%), Gaps = 13/238 (5%)  
Strand=Plus/Plus

Query 1 TGAAGGTTGGGTAAACACTCCGGCCTCTAGGCCATTCCCTCTttttttttgttttt  
Sbjct 9387 .....A.....G.-.....-

>gb|AF177039.1| Synthetic construct clone pH77-J6S hepatitis C virus, comp genome

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Score = 300 bits (162), Expect = 2e-78  
Identities = 215/238 (90%), Gaps = 13/238 (5%)  
Strand=Plus/Plus

>gb|AF177038.1| Synthetic construct clone pH77(p7)CV-J6S hepatitis C virus genome  
Length=9611

Score = 300 bits (162), Expect = 2e-78  
Identities = 215/238 (90%), Gaps = 13/238 (5%)  
Strand=Plus/Plus

Query Sbjct	1 9387	TGAAGGTTGGGGTAAACACTCCGGCCTCTTAGGCCATTCCCTCTCttttttttgtttttt .....A.....G.-.....-
Query Sbjct	61 9445	tgggtttttttgtttttttcttt ---.....-.....C.-.....C..CC..C..C..C..--..-..-..-..
Query Sbjct	121 9495	ctcttttttcttcTTAATGGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAA -.....CC.....
Query Sbjct	181 9554	GGTCCGTGAGCCGCATGACTGCAGAGAGTGCTGATACTGGCCTCTGCAGATCATGT .....

>gb|AF177037.1| Synthetic construct clone pH77CV-J6S hepatitis C virus, complete genome  
Length=9611

Score = 300 bits (162), Expect = 2e-78  
Identities = 215/238 (90%), Gaps = 13/238 (5%)  
Strand=Plus/Plus

>gb|AF011753.1|AF011753 Hepatitis C virus strain H77 pH21 polyprotein gene  
cds  
Length=9599

Score = 300 bits (162), Expect = 2e-78  
Identities = 215/238 (90%), Gaps = 13/238 (5%)  
Strand=Plus/Plus

>gb|AF011752.1|AF011752 Hepatitis C virus strain H77 pCV-H11 polyprotein g  
p://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi 6/25/07

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cds  
Length=9599

Score = 300 bits (162), Expect = 2e-78  
Identities = 215/238 (90%), Gaps = 13/238 (5%)  
Strand=Plus/Plus

>gb|AF011751.1|AF011751 Hepatitis C virus strain H77 pCV-H77C polyprotein  
cds  
Length=9599

Score = 300 bits (162), Expect = 2e-78 .  
Identities = 215/238 (90%), Gaps = 13/238 (5%)  
Strand=Plus/Plus

>gb|AY045702.1| Hepatitis C virus isolate HCR6, complete genome  
Length=9611

Score = 296 bits (160), Expect = 2e-77  
Identities = 206/228 (90%), Gaps = 4/228 (1%)  
Strand=Plus/Plus

>gb|AF139594.2| Hepatitis C virus strain HCV-N, complete genome  
Length=9616

Score = 294 bits (159), Expect = 8e-77  
Identities = 209/230 (90%), Gaps = 16/230 (6%)  
Strand=Plus/Plus

# WEST Search History

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DATE: Monday, June 25, 2007

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>			
<input type="checkbox"/>	L16	L15 and l9	162
<input type="checkbox"/>	L15	restriction same (subclon\$ or sub adj clon\$4) and substitution with restriction	682
<input type="checkbox"/>	L14	L12 and l10	2
<input type="checkbox"/>	L13	L12 amd l10	16840
<input type="checkbox"/>	L12	l9 and replicon same (virus or viral)	34
<input type="checkbox"/>	L11	l9 and replicon same (HCV or hepatitis adj c)	1
<input type="checkbox"/>	L10	L9 and restriction same (replicon or vector) same (silent)	83
		substitution same restriction same (amino adj acid or coding or silent)	
<input type="checkbox"/>	L9	and (@ad<2000416 or @pd<20020416) and restriction same (replicon or vector)	1014
<input type="checkbox"/>	L8	l6 and substitution same restriction same (amino adj acid or coding or silent)	11
<input type="checkbox"/>	L7	l6 and (@ad<2000416 or @pd<20020416)	2
<input type="checkbox"/>	L6	(HCV or hepatitis adj C) same replicon and replicon same restriction same site	69
<input type="checkbox"/>	L5	(HCV or hepatitis adj C) same replicon and restriction same site	241
<input type="checkbox"/>	L4	L3 and (@ad<2000416 or @pd<20020416)	3
<input type="checkbox"/>	L3	L1 and L2	153
<input type="checkbox"/>	L2	(HCV or hepatitis adj C) same replicon AND (UTR or 3') same (1a or H77)	180
<input type="checkbox"/>	L1	(HCV or hepatitis adj C) same replicon AND (replicon or HCV or virus) same (1a or H77)	223

END OF SEARCH HISTORY